



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: MELKI, JUDITH
MUNNICH, ARNOLD

(ii) TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
FOR SPINAL MUSCULAR ATROPHY

(iii) NUMBER OF SEQUENCES: 65

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/545,196
(B) FILING DATE: 19-OCT-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: FARACI, C. J.
(B) REGISTRATION NUMBER: 32,350
(C) REFERENCE/DOCKET NUMBER: 2121-110P

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTTTAAA TTTTTGTAG AGACAGGGTC TCATTATGTT SCCCAGGGTG GTGTCAAGCT

60

- CCAGGTCTCA AGTGATCCCC CTACCTCCGC CTCCCAAAGT TGTGGGATTG TAGGCATGAG

120

CCACTGCAAG AAAACCTTAA CTGCAGCCTA ATAATTGTT TCTTGGGAT AACTTTAAA	180
GTACATTAAG AGACTATCAA CTTAATTCT GATCATATT TGTTGAATAA AATAAGTAAA	240
ATGTCTTGTG AACAAAATGC TTTTAACAT CCATATAAAG CTATCTATAT ATAGCTATCT	300
ATGTCTATAT AGCTATTTT TTTAACCTCC TTTTATTTTC CTTACAG	347

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTAAGTCTGC CAGCATTATG AAAGTGAATC TACTTTGT AAAACTTAT GTTTGTGGA	60
AAACAAATGT TTTGAACAG TAAAAAGTT CAGATGTTAA AAAGTTGAAA GTTAAATGTA	120
AAACAATCAA TATTAAGAA TTTGATGCC AAAACTATTA GATAAAAGGT TAATCTACAT	180
CCCTACTAGA ATTCTCATAAC TTAACTGGTT GTTATGTGG AAGAACATA CTTTCACAAT	240
AAAGAGCTT AGGATATGAT GCCATTTAT ATCACTAGTA GGCAGACCAG CAGACTTTT	300
TTTATTGTGA TATGGGATAA CCTAGGCATA CTGCACTGTA CACTCTGACA TATGAAGTGC	360
TCTAGTCAAG TTTAACTGGT GTCCACAGAG GACATGGTT AACTGGAATT CGTCAAGCCT	420
CTGGTTCTAA TTTCTCATTG GCAG	444

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AATTTTAAATTTTGAG AGACAGGGTC TCATTATGTT GCCCAGGGTG GTGTCAAGCT	60
CGAGGTCTCA AGTGATCCCC CTACCTCCGC CTCCCAAAGT TGTGGGATTG TAGGCATGAG	120
CCACTGCAAG AAAACCTTAA CTGCAGCCTA ATAATTGTT TCTTGGGAT AACTTTAAA	180
GTAATTAAG AGACTATCAA CTTAATTCT GATCATATT TGTTGAATAA AATAAGTAAA	240

ATGTCTTGTG AACAAAATGC TTTTTAACAT CCATATAAAG CTATCTATAT ATAGCTATCT	300
ATATCTATAT AGCTATTTT TTTAACCC TTTTATTTTC CTTACAG	347

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTAAGTCTGC CAGCATTATG AAAGTGAATC TTACTTTGT AAAACTTAT GGTTGTGGA	60
AAAACAAATGT TTTTGAACAG TTAAAAAGTT CAGATGTTAG AAAGTTGAAA GGTAAATGTA	120
AAACAATCAA TATTAAAGAA TTTTGATGCC AAAACTATTAA GATAAAAGGT TAATCTACAT	180
CCCTACTAGA ATTCTCATAAC TTAACTGGTT GGTTGTGTGG AAGAAACATA CTTTCACAAT	240
AAAGAGCTTT AGGATATGAT GCCATTTAT ATCACTAGTA GGCAGACCAG CAGACTTTT	300
TTTATTGTGA TATGGGATAA CCTAGGCATA CTGCACTGTA CACTCTGACA TATGAAGTGC	360
TCTAGTCAAG TTTAACTGGT GTCCACAGAG GACATGGTTT AACTGGAATT CGTCAAGCCT	420
CTGGTTCTAA TTTCTCATTG GCAG	444

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "SYNTHETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGACTATCAA CTTAATTCT GATCA	25
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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "SYNTHETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TAAGGAATGT GAGCACCTTC CTTC

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "SYNTHETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTAATAACCA AATGCAATGT GAA

23

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "SYNTHETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTACAACACC CTTCTCACAG

20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 294 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Met Ser Ser Gly Gly Ser Gly Gly Gly Val Pro Glu Gln Glu
 1 5 10 15

Asp Ser Val Leu Phe Arg Arg Gly Thr Gly Gln Ser Asp Asp Ser Asp
 20 25 30

Ile Trp Asp Asp Thr Ala Leu Ile Lys Ala Tyr Asp Lys Ala Val Ala
 35 40 45

Ser Phe Lys His Ala Leu Lys Asn Gly Asp Ile Cys Glu Thr Ser Gly
 50 55 60

Lys Pro Lys Thr Thr Pro Lys Arg Lys Pro Ala Lys Lys Asn Lys Ser
 65 70 75 80

Gln Lys Lys Asn Thr Ala Ala Ser Leu Gln Gln Trp Lys Val Gly Asp
 85 90 95

Lys Cys Ser Ala Ile Trp Ser Glu Asp Gly Cys Ile Tyr Pro Ala Thr
 100 105 110

Ile Ala Ser Ile Asp Phe Lys Arg Glu Thr Cys Val Val Val Tyr Thr
 115 120 125

Gly Tyr Gly Asn Arg Glu Glu Gln Asn Leu Ser Asp Leu Leu Ser Pro
 130 135 140

Ile Cys Glu Val Ala Asn Asn Ile Glu Gln Asn Ala Gln Glu Asn Glu
 145 150 155 160

Asn Glu Ser Gln Val Ser Thr Asp Glu Ser Glu Asn Ser Arg Ser Pro
 165 170 175

Gly Asn Lys Ser Asp Asn Ile Lys Pro Lys Ser Ala Pro Trp Asn Ser
 180 185 190

Phe Leu Pro Pro Pro Pro Met Pro Gly Pro Arg Leu Gly Pro Gly
 195 200 205

Lys Pro Gly Leu Lys Phe Asn Gly Pro Pro Pro Pro Pro Pro Pro Pro
 210 215 220

Pro Pro His Leu Leu Ser Cys Trp Leu Pro Pro Phe Pro Ser Gly Pro
 225 230 235 240

Pro Ile Ile Pro Pro Pro Pro Ile Cys Pro Asp Ser Leu Asp Asp
 245 250 255

Ala Asp Ala Leu Gly Ser Met Leu Ile Ser Trp Tyr Met Ser Gly Tyr
 260 265 270

His Thr Gly Tyr Tyr Met Gly Phe Arg Gln Asn Gln Lys Glu Gly Arg
 275 280 285

Cys Ser His Ser Leu Asn
 290

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii). MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGGGCCCA CGCTGCGCAC CCGCGGTTT GCTATGGCGA TGAGCAGCGG CGGCAGTGGT	60
GGCGGCGTCC CGGAGCAGGA GGATTCCGTG CTGTTCCGGC GCGGCACAGG CCAGAGCGAT	120
GATTCTGACA TTTGGGATGA TACAGCACTG ATAAAAGCAT ATGATAAAGC TGTGGCTTCA	180
TTTAAGCATG CTCTAAAGAA TGGTGACATT TGTGAAACTT CGGGTAAACC AAAAACACAA	240
CCTAAAAGAA AACCTGCTAA GAAGAATAAA AGCCAAAAGA AGAATACTGC AGCTTCCTTA	300
CAACAGTGGA AAGTTGGGA CAAATGTTCT GCCATTGGT CAGAAGACGG TTGCATTTAC	360
CCAGCTACCA TTGCTTCAAT TGATTTAAG AGAGAAACCT GTGTTGTGGT TTACACTGGA	420
TATGGAAATA GAGAGGAGCA AAATCTGTCC GATCTACTTT CCCCCAATCTG TGAAGTAGCT	480
AATAATATAG AACAGAATGC TCAAGAGAAT GAAAATGAAA GCCAAGTTTC AACAGATGAA	540
AGTGAGAACT CCAGGTCTCC TGGAAATAAA TCAGATAACA TCAAGCCAA ATCTGCTCCA	600
TGGAACCCCT TTCTCCCTCC ACCACCCCCC ATGCCAGGGC CAAGACTGGG ACCAGGAAAG	660
CCAGGTCTAA AATTCAATGG CCCACCACCG CCACCGCCAC CACCACCAAC CCACTTACTA	720
TCATGCTGGC TGCCTCCATT TCCTTCTGGA CCACCAATAA TTCCCCCACC ACCTCCATA	780
TGTCCAGATT CTCTTGATGA TGCTGATGCT TTGGGAAGTA TGTTAATTTC ATGGTACATG	840
AGTGGCTATC ATACTGGCTA TTATATGGGT TTTAGACAAA ATCAAAAAGA AGGAAGGTGC	900
TCACATTCCCT TAAATTAAGG AGAAATGCTG GCATAGAGCA GCACTAAATG ACACCACTAA	960
AGAAACGATC AGACAGATCT GGAATGTGAA GCGTTATAGA AGATAACTGG CCTCATTCT	1020
TCAAAATATC AAGTGTGGG AAAGAAAAAA GGAAGTGGAA TGGGTAACTC TTCTTGATTA	1080
AAAGTTATGT AATAACCAAA TGCAATGTGA AATATTTAC TGGACTCTTT TGAAAAACCA	1140
TCTGTAAAAG ACTGAGGTGG GGGTGGGAGG CCAGCACGGT GGTGAGGCAG TTGAGAAAAT	1200
TTGAATGTGG ATTAGATTT GAATGATATT GGATAATTAT TGGTAATTTT ATGGCCTGTG	1260
AGAAGGGTGT TGTAGTTAT AAAAGACTGT CTTAATTGCA ATACTTAAGC ATTTAGGAAT	1320
GAAGTGTAG AGTGTCTAA AATGTTCAA ATGGTTAAC AAAATGTATG TGAGGCGTAT	1380
GTGGCAAAAT GTTACAGAAT CTAACGGTG GACATGGCTG TTCATTGTAC TGTTTTTTC	1440
TATCTTCTAT ATGTTAAAAA GTATATAATA AAAATATTAA ATTTTTTTT AAAAAAA	1500

AAAAAAAAAA	1560						
AAAAAAAAAA	AAAAAAAAAA	AA					1582

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AATTTTAAA	TTTTTGTAG	AGACAGGGTC	TCATTATGTT	GCCCAGGGTG	GTGTCAAGCT	60
CCAGGTCTCA	AGTGATCCCC	CTACCTCCGC	CTCCCAAAGT	TGTGGGATTG	TAGGCATGAG	120
CCACTGCAAG	AAAACCTTAA	CTGCAGCCTA	ATAATTGTTT	TCTTTGGGAT	AACTTTAAA	180
GTACATTTAAA	AGACTATCAA	CTTAATTCT	GATCATATT	TGTTGAATAA	AATAAGTAAA	240
ATGTCTTGTG	AACAAAATGC	TTTTAACAT	CCATATAAAG	CTATCTATAT	ATAGCTATCT	300
ATATCTATAT	AGCTATTTT	TTTAACCTCC	TTTATTTTC	CTTACAGGGT	TTTAGACAAA	360
ATCAAAAAGA	AGGAAGGTGC	TCACATTCC	TAAATTAAGG	AGTAAGTCTG	CCAGCATTAT	420
GAAAGTGAAT	CTTACTTTG	TAAAACTTA	TGGTTGTGG	AAAACAAATG	TTTTGAACA	480
GTTAAAAAGT	TCAGATGTTA	GAAAGTTGAA	AGGTTAATGT	AAAACAATCA	ATATTAAAGA	540
ATTTGATGC	CAAAACTATT	AGATAAAAGG	TTAATCTACA	TCCCTACTAG	AATTCTCATA	600
CTTAACTGGT	TGGTTGTGTG	GAAGAAACAT	ACTTCACAA	TAAAGAGCTT	TAGGATATGA	660
TGCCATTTA	TATCACTAGT	AGGCAGACCA	GCAGACTTT	TTTATTGTG	ATATGGGATA	720
ACCTAGGCAT	ACTGCACTGT	ACACTCTGAC	ATATGAAGTG	CTCTAGTCAA	GTTTAACTGG	780
TGTCCACAGA	GGACATGGTT	TAACGGAAT	TCGTCAAGCC	TCTGGTTCTA	ATTTCTCATT	840
TGCAGGAAAT	GCTGGCATAG	AGCAGCACTA	AATGACACCA	CTAAAGAAC	GATCAGACAG	900
ATCTGGAATG	TGAAGCGTTA	TAGAAGATAA	CTGGCCTCAT	TTCTTCAAAA	TATCAAGTGT	960
TGGGAAAGAA	AAAAGGAAGT	GGAATGGGT	ACTCTTCTTG	ATTAAAAGTT	ATGTAATAAC	1020
CAAATGCAAT	GTGAAATATT	TTACTGGACT	CTTTGAAAA	ACCATCTGTA	AAAGACTGAG	1080
GTGGGGGTGG	GAGGCCAGCA	CGGTGGTGAG	GCAGTTGAGA	AAATTGAAAT	GTGGATTAGA	1140
TTTTGAATGA	TATTGGATAA	TTATTGGTAA	TTTTATGGCC	TGTGAGAAGG	GTGTTGTAGT	1200
TTATAAAAAGA	CTGTCTTAAT	TTGCATACTT	AAGCATTAG	GAATGAAGTG	TTAGAGTGTC	1260

TTAAAATGTT TCAAATGGTT TAACAAAATG TATGTGAGGC GTATGTGGCA AAATGTTACA	1320
GAATCTAACT GGTGGACATG GCTGTTCACT GTACTGTTTT TTTCTATCTT CTATATGTT	1380
AAAAGTATAT AATAAAAATA TTTAATT	1408

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGGGGCCCCA CGCTGCGCAT CCGCGGGTTT GCTATGGCGA TGAGCAGCGG CGGCAGTGGT	60
GGCGGCGTCC CGGAGCAGGA GGATTCCGTG CTGTTCCGGC GCGGCACAGG CCAGAGCGAT	120
GATTCTGACA TTTGGGATGA TACAGCACTG ATAAAAGCAT ATGATAAAGC TGTGGCTTCA	180
TTTAAGCATG CTCTAAAGAA TGGTGACATT TGTGAAACTT CGGGTAAACC AAAAACACAA	240
CCTAAAGAA AACCTGCTAA GAAGAATAAA AGCCAAAAGA AGAATACTGC AGCTTCCTTA	300
CAACAGTGGAA AAGTTGGGAA CAAATGTTCT GCCATTTGGT CAGAAGACGG TTGCATTAC	360
CCAGCTACCA TTGCTTCAAT TGATTTAAG AGAGAAACCT GTGTTGTGGT TTACACTGGA	420
TATGGAAATA GAGAGGAGCA AAATCTGTCC GATCTACTTT CCCCAATCTG TGAAGTAGCT	480
AATAATATAG AACAGAATGC TCAAGAGAAT GAAAATGAAA GCCAAGTTTC AACAGATGAA	540
AGTGAGAACT CCAGGTCTCC TGGAAATAAA TCAGATAACA TCAAGCCAA ATCTGCTCCA	600
TGGAACTCTT TTCTCCCTCC ACCACCCCCC ATGCCAGGGC CAAGACTGGG ACCAGGAAAG	660
CCAGGTCTAA AATTCAATGG CCCACCACCG CCACCGCCAC CACCACCAAC CCACCTACTA	720
TCATGCTGGC TGCCTCCATT TCCTTCTGGA CCACCAATAA TTCCCCCACC ACCTCCCATA	780
TGTCCAGATT CTCTTGATGA TGCTGATGCT TTGGGAAGTA TGTTAATTTC ATGGTACATG	840
AGTGGCTATC ATACTGGCTA TTATATGGGT TTCAGACAAA ATCAAAAAGA AGGAAGGTGC	900
TCACATTCCCT TAAATTAAGG AGAAATGCTG GCATAGAGCA GCACTAAATG ACACCACTAA	960
AGAAACGATC AGACAGATCT GGAATGTGAA GCGTTATAGA AGATAACTGG CCTCATTCT	1020
TCAAAATATC AAGTGTGGG AAAGAAAAAA GGAAGTGGAA TGGGTAACTC TTCTTGATTA	1080
AAAGTTATGT AATAACCAAA TGCAATGTGA AATATTTAC TGGACTCTTT TGAAAAACCA	1140
TCTGTAAAAG ACTGGGGTGG GGGTGGGAGG CCAGCACGGT GGTGAGGCAG TTGAGAAAAT	1200

TTGAATGTGG ATTAGATTTT GAATGATATT GGATAATTAT TGGTAATTTT ATGGCCTGTG	1260
AGAAGGGTGT TGTAGTTAT AAAAGACTGT CTTAATTGC ATACTTAAGC ATTTAGGAAT	1320
GAAGTGTAG AGTGTCTAA AATGTTCAA ATGGTTAAC AAAATGTATG TGAGGCGTAT	1380
GTGGCAAAAT GTTACAGAAT CTAACGGTG GACATGGCTG TTCATTGTAG TGTTTTTC	1440
TATCTTCTAT ATGTTAAAAA GTATATAATA AAAATATTTA ATTTTTTTT AAAAAAAA	1500
AAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	1560
AAAAAAA AAAAAAAA AA	1582

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AATTTTAAA TTTTTGTAG AGACAGGGTC TCATTATGTT GCCCAGGGTG GTGTCAAGCT	60
CCAGGTCTCA AGTGATCCCC CTACCTCCGC CTCCCAAAGT TGTGGGATTG TAGGCATGAG	120
CCACTGCAAG AAAACCTAA CTGCAGCCTA ATAATTGTT TCTTGGGAT AACTTTAAA	180
GTACATTAAA AGACTATCAA CTTAATTCT GATCATATT TGTTGAATAA AATAAGTAAA	240
ATGTCTTGTG AACAAAATGC TTTTAACAT CCATATAAG CTATCTATAT ATAGCTATCT	300
ATGTCTATAT AGCTATTTT TTTAACTTCC TTTTATTTTC CTTACAGGGT TTCAGACAAA	360
ATCAAAAAGA AGGAAGGTGC TCACATTCCCT TAAATTAAGG AGTAAGTCTG CCAGCATTAT	420
GAAAGTGAAT CTTACTTTG TAAAACTTA TGGTTGTGG AAAACAAATG TTTTGAAACA	480
GTTAAAAAGT TCAGATGTTA AAAAGTTGAA AGGTTAATGT AAAACAATCA ATATTAAGA	540
ATTTGATGC CAAAACATT AGATAAAAGG TTAATCTACA TCCCTACTAG AATTCTCATA	600
CTTAACGGT TGGTTATGTG GAAGAACAT ACTTTCACAA TAAAGAGCTT TAGGATATGA	660
TGCCATTTA TATCACTAGT AGGCAGACCA GCAGACTTT TTTTATTGTG ATATGGATA	720
ACCTAGGCAT ACTGCACTGT ACACCTGAC ATATGAAGTG CTCTAGTCAC GTTTAACTGG	780
TGTCCACAGA GGACATGGTT TAACTGGAAT TCGTCAAGCC TCTGGTTCTA ATTTCTCATT	840
TGCAGGAAAT GCTGGCATAG AGCAGGACTA AATGACACCA CTAAAGAAC GATCAGACAG	900
ATCTGGAATG TGAAGCGTTA TAGAAGATAA CTGGCCTCAT TTCTTCAAAA TATCAAGTGT	960

TGGGAAAGAA AAAAGGAAGT GGAATGGTA ACTCTTCTT ATTAAAAGTT ATGTAATAAC	1020
CAAATGCAAT GTGAAATATT TTACTGGACT CTTTGAAAA ACCATCTGTA AAAGACTGGG	1080
GTGGGGGTGG GAGGCCAGCA CGGTGGTGAG GCAGTTGAGA AAATTTGAAT GTGGATTAGA	1140
TTTGAAATGA TATTGGATAA TTATTGGTAA TTTTATGCC TGTGAGAAGG GTGTTGTAGT	1200
TTATAAAAAGA CTGTCTTAAT TTGCATACTT AAGCATTAG GAATGAAGTG TTAGAGTGT	1260
TTAAAATGTT TCAAATGGTT TAACAAAATG TATGTGAGGC GTATGTGGCA AAATGTTACA	1320
GAATCTAACT GGTGGACATG GCTGTTCATT GTACTGTTT TTTCTATCTT CTATATGTTT	1380
AAAAGTATAT AATAAAAATA TTTAATT	1408

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACCTGANCCC AGANGGTCAAG GCTGCAGTG AGACGAGATT GCNCCACTGC CCTCCACCT	60
GGGTGATAAG AGTGGGACCC TGTNTCAAAA CATAACACACA CACACACACA CACACACACA	120
CACACACACA CACACTCTCT CTCTCTCTCT CTCTCTCTCT CTCTCTCTCA	180
AAAACACTTG GTCTGTTATT TTTNCGAAAT TGTCAGTCAT AGTTATCTGT TAGACCAAAG	240
CTGNGTAAGN ACATTTATTA CATTGCCTCC TACAACTTCA TCAGCTAATG TATTTGCTAT	300
ATAGCAATTA CATATNGGNA TATATTATCT TNAGGGGATG GCCANGTNAT AAAACTGTCA	360
CTGAGGAAAG GA	372

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCCCACCT NAGCCTCCCC AGTAGCTAGG ACTATAGGCG TGCNCCACCA AGCTCAGCTA	60
TTTTTNNTAT TTAGTAGAGA CGGGGTTTCG GCANGCTTAG GCCTCGTNTC GAACTCCAGT	120
GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT AGATATTTAT	180
TCCCCCTCCC CCTTGGAAAA GTAAGTAAGC TCCTACTAGG AATTAAAAC CTGCTTGATC	240
TATATAAAGA CAAACAAGGA AAGACAAACA TGGGGGCAGG AAGGAAGGCA GATC	294

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCGAGGTAGA TTTGTATTAT ATCCCATGTA CACACACACA CACACACACA CACACACACA	60
CACACACAGA CTTAATCTGT TTACAGAAAT AAAAGGAATA AAATACCGTT TCTACTATAC	120
ACCAAAACTA GCCATCTTGA C	141

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCTGAGAAG GCTTCCTCCT GAGTATGCAT AAACATTACAG AGCTTGCATG CGTGTGTGTG	60
TGTGTGTGTG TGTGTATGTT TGCTTGCCT GTAAAAACAA TTGCAACATC AACAGAAATA	120
AAAATTAAG GAATAATTCT CCTCCGACTC TGCCGTTCCA TCCAGTGAAA CTCTTCATTC	180
TGGGGTAAAG TTCCTTCAGT TCTTTCATAG ATAGGTATAT ACTTCATAAG TCAAACAATC	240
AGGCTGGGTG CAGTAGCTCA TGCCCTGTAAT CCCAGCCCTT TGGGAGGCCG AGCTGGGCAG	300

ATCGA

305

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCCACCCGCC TTGGCCTCCC AAAGCCTGG GATTACAGGC GTGACTGCCG CACCCAGCTG	60
TAAACTGGNT TNNTAATGGT AGATTTNAG GTATTAACAA TAGATAAAAAA GATACTTTN	120
GGCATACTGT GTATTGGGAT GGGGTTAGAA CAGGTGTNCT ACCCAAGACA TTTACTTAAA	180
ATCGCCCTCG AAATGCTATG TGAGCTGTGT GTGTGTGTGT GTGTGTGTGT GTATTAAGGA	240
AAAGCATGAA AGTATTTATG CTTGATTTT TTTTTNACT CATAGCTTCA TAGTGGANCA	300
GATACATAGT CTAAATCAAA ATGTTAAC TTTTATGTC ACTTGCTGTC	350

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ala Met Ser Ser Gly Gly Ser Gly Gly Val Pro Glu Gln Glu			
1	5	10	15
Asp Ser Val Leu Phe Arg Arg Gly Thr Gly Gln Ser Asp Asp Ser Asp			
20	25	30	
Ile Trp Asp Asp Thr Ala Leu Ile Lys Ala Tyr Asp Lys Ala Val Ala			
35	40	45	
Ser Phe Lys His Ala Leu Lys Asn Gly Asp Ile Cys Glu Thr Ser Gly			
50	55	60	
Lys Pro Lys Thr Thr Pro Lys Arg Lys Pro Ala Lys Lys Asn Lys Ser			
65	70	75	80
Gln Lys Lys Asn Thr Ala Ala Ser Leu Gln Gln Trp Lys Val Gly Asp			

85	90	95
Lys Cys Ser Ala Ile Trp Ser Glu Asp Gly Cys Ile Tyr Pro Ala Thr		
100	105	110
Ile Ala Ser Ile Asp Phe Lys Arg Glu Thr Cys Val Val Val Tyr Thr		
115	120	125
Gly Tyr Gly Asn Arg Glu Glu Gln Asn Leu Ser Asp Leu Leu Ser Pro		
130	135	140
Ile Cys Glu Val Ala Asn Asn Ile Glu Gln Asn Ala Gln Glu Asn Glu		
145	150	155
Asn Glu Ser Gln Val Ser Thr Asp Glu Ser Glu Asn Ser Arg Ser Pro		
165	170	175
Gly Asn Lys Ser Asp Asn Ile Lys Pro Lys Ser Ala Pro Trp Asn Ser		
180	185	190
Phe Leu Pro Pro Pro Pro Met Pro Gly Pro Arg Leu Gly Pro Gly		
195	200	205
Lys Pro Gly Leu Lys Phe Asn Gly Pro Pro Pro Pro Pro Pro Pro		
210	215	220
Pro Pro His Leu Leu Ser Cys Trp Leu Pro Pro Phe Pro Ser Gly Pro		
225	230	235
Pro Ile Ile Pro Pro Pro Pro Ile Cys Pro Asp Ser Leu Asp Asp		
245	250	255
Ala Asp Ala Leu Gly Ser Met Leu Ile Ser Trp Tyr Met Ser Gly Tyr		
260	265	270
His Thr Gly Tyr Tyr Met		
275		

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 18..881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGGCGTGGTA GCAGGCC ATG GCG ATG GGC AGT GGC GGA GCG GGC TCC GAG	50	
Met Ala Met Gly Ser Gly Gly Ala Gly Ser Glu		
1	5	10

CAG GAA GAT ACG GTG CTG TTC CGG CGT GGC ACC GGC CAG AGT GAT GAT	98
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Gln	Glu	Asp	Thr	Val	Leu	Phe	Arg	Arg	Gly	Thr	Gly	Gln	Ser	Asp	Asp		
15																	
TCT	GAC	ATT	TGG	GAT	ACA	GCA	TTG	ATA	AAA	GCT	TAT	GAT	AAA	GCT		146	
Ser	Asp	Ile	Trp	Asp	Asp	Thr	Ala	Leu	Ile	Lys	Ala	Tyr	Asp	Lys	Ala		
30																40	
GTG	GCT	TCC	TTT	AAG	CAT	GCT	CTA	AAG	AAC	GGT	GAC	ATT	TGT	GAA	ACT		194
Val	Ala	Ser	Phe	Lys	His	Ala	Leu	Lys	Asn	Gly	Asp	Ile	Cys	Glu	Thr		
45																55	
CCA	GAT	AAG	CCA	AAA	GGC	ACA	GCC	AGA	AGA	AAA	CCT	GCC	AAG	AAG	AAT		242
Pro	Asp	Lys	Pro	Lys	Gly	Thr	Ala	Arg	Arg	Lys	Pro	Ala	Lys	Lys	Asn		
60																75	
AAA	AGC	CAA	AAG	AAG	AAT	GCC	ACA	ACT	CCC	TTG	AAA	CAG	TGG	AAA	GTT		290
Lys	Ser	Gln	Lys	Lys	Asn	Ala	Thr	Thr	Pro	Leu	Lys	Gln	Trp	Lys	Val		
80																90	
GGT	GAC	AAG	TGT	TCT	GCT	GTT	TGG	TCA	GAA	GAC	GGC	TGC	ATT	TAC	CCA		338
Gly	Asp	Lys	Cys	Ser	Ala	Val	Trp	Ser	Glu	Asp	Gly	Cys	Ile	Tyr	Pro		
95																105	
GCT	ACT	ATT	ACG	TCC	ATT	GAC	TTT	AAG	AGA	GAA	ACC	TGT	GTC	GTC	GTT		386
Ala	Thr	Ile	Thr	Ser	Ile	Asp	Phe	Lys	Arg	Glu	Thr	Cys	Val	Val	Val		
110																120	
TAT	ACT	GGA	TAT	GGA	AAC	AGA	GAG	GAG	CAA	AAC	TTA	TCT	GAC	CTA	CTT		434
Tyr	Thr	Gly	Tyr	Gly	Asn	Arg	Glu	Glu	Gln	Asn	Leu	Ser	Asp	Leu	Leu		
125																135	
TCC	CCG	ACC	TGT	GAA	GTA	GCT	AAT	AGT	ACA	GAA	CAG	AAC	ACT	CAG	GAG		482
Ser	Pro	Thr	Cys	Glu	Val	Ala	Asn	Ser	Thr	Glu	Gln	Asn	Thr	Gln	Glu		
140																155	
AAT	GAA	AGT	CAA	GTT	TCC	ACA	GAC	GAC	AGT	GAA	CAC	TCC	TCC	AGA	TCG		530
Asn	Glu	Ser	Gln	Val	Ser	Thr	Asp	Asp	Ser	Glu	His	Ser	Ser	Arg	Ser		
150																170	
CTC	AGA	AGT	AAA	GCA	CAC	AGC	AAG	TCC	AAA	GCT	GCT	CCG	TGG	ACC	TCA		578
Leu	Arg	Ser	Lys	Ala	His	Ser	Lys	Ser	Lys	Ala	Ala	Pro	Trp	Thr	Ser		
175																185	
TTT	CTT	CCT	CCA	CCA	CCC	CCA	ATG	CCA	GGG	TCA	GGA	TTA	GGA	CCA	GGA		626
Phe	Leu	Pro	Pro	Pro	Pro	Pro	Met	Pro	Gly	Ser	Gly	Leu	Gly	Pro	Gly		
190																195	
AAG	CCA	GGT	CTA	AAA	TTC	AAC	GGC	CCG	CCG	CCG	CCG	CCT	CCA	CTA	CCC		674
Lys	Pro	Gly	Leu	Lys	Phe	Asn	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro		
205																210	
CCT	CCC	CCC	TTC	CTG	CCG	TGC	TGG	ATG	CCC	CCG	TTC	CCT	TCA	GGA	CCA		722
Pro	Pro	Pro	Phe	Leu	Pro	Cys	Trp	Met	Pro	Pro	Phe	Pro	Ser	Gly	Pro		
220																225	
CCA	ATA	ATC	CCG	CCA	CCC	CCT	CCC	ATC	TCT	CCC	GAC	TGT	CTG	GAT	GAC		770
Pro	Ile	Ile	Pro	Pro	Pro	Pro	Pro	Ile	Ser	Pro	Asp	Cys	Leu	Asp	Asp		
240																245	
ACT	GAT	GCC	CTG	GGC	AGT	ATG	CTA	ATC	TCT	TGG	TAC	ATG	AGT	GGC	TAC		818
Thr	Asp	Ala	Leu	Gly	Ser	Met	Leu	Ile	Ser	Trp	Tyr	Met	Ser	Gly	Tyr		

255

260

265

CAC ACT GGC TAC TAT ATG GGT TTC AGA CAA AAT AAA AAA GAA GGA AAG
 His Thr Gly Tyr Tyr Met Gly Phe Arg Gln Asn Lys Lys Glu Gly Lys
 270 275 280

866

TGC TCA CAT ACA AAT TAAG
 Cys Ser His Thr Asn
 285

885

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ala Met Gly Ser Gly Gly Ala Gly Ser Glu Gln Glu Asp Thr Val
 1 5 10 15

Leu Phe Arg Arg Gly Thr Gly Gln Ser Asp Asp Ser Asp Ile Trp Asp
 20 25 30

Asp Thr Ala Leu Ile Lys Ala Tyr Asp Lys Ala Val Ala Ser Phe Lys
 35 40 45

His Ala Leu Lys Asn Gly Asp Ile Cys Glu Thr Pro Asp Lys Pro Lys
 50 55 60

Gly Thr Ala Arg Arg Lys Pro Ala Lys Lys Asn Lys Ser Gln Lys Lys
 65 70 75 80

Asn Ala Thr Thr Pro Leu Lys Gln Trp Lys Val Gly Asp Lys Cys Ser
 85 90 95

Ala Val Trp Ser Glu Asp Gly Cys Ile Tyr Pro Ala Thr Ile Thr Ser
 100 105 110

Ile Asp Phe Lys Arg Glu Thr Cys Val Val Val Tyr Thr Gly Tyr Gly
 115 120 125

Asn Arg Glu Glu Gln Asn Leu Ser Asp Leu Leu Ser Pro Thr Cys Glu
 130 135 140

Val Ala Asn Ser Thr Glu Gln Asn Thr Gln Glu Asn Glu Ser Gln Val
 145 150 155 160

Ser Thr Asp Asp Ser Glu His Ser Ser Arg Ser Leu Arg Ser Lys Ala
 165 170 175

His Ser Lys Ser Lys Ala Ala Pro Trp Thr Ser Phe Leu Pro Pro Pro
 180 185 190

Pro Pro Met Pro Gly Ser Gly Leu Gly Pro Gly Lys Pro Gly Leu Lys
 195 200 205

Phe Asn Gly Pro Phe Leu
 210 215 220

Pro Cys Trp Met Pro Pro Phe Pro Ser Gly Pro Pro Ile Ile Pro Pro
 225 230 235 240

Pro Pro Pro Ile Ser Pro Asp Cys Leu Asp Asp Thr Asp Ala Leu Gly
 245 250 255

Ser Met Leu Ile Ser Trp Tyr Met Ser Gly Tyr His Thr Gly Tyr Tyr
 260 265 270

Met Gly Phe Arg Gln Asn Lys Lys Glu Gly Lys Cys Ser His Thr Asn
 275 280 285

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 104..184

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 364..435

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 637..756

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 921..1121

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1265..1417

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1605..1700

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1810..1920

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2214..2261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCTCCCGGGC ACCGTACTGT TCCGCTCCCA GAAGCCCCGG GCGCCGGAAG TCGTCACTCT	60
TAAGAAGGGA CGGGGCCCCA CGCTGCCAC CCCGGGGTTT GCT ATG GCG ATG AGC Met Ala Met Ser	115
1	
AGC GGC GGC AGT GGT GGC GGC GTC CCG GAG CAG GAG GAT TCC GTG CTG Ser Gly Gly Ser Gly Gly Val Pro Glu Gln Glu Asp Ser Val Leu	163
5 10 15 20	
TTC CGG CGC GGC ACA GGC CAG GTGAGGTCGC AGCCAGTGCA GTCTCCCTAT Phe Arg Arg Gly Thr Gly Gln	214
25	
TAGCGCTCTC AGCACCCCTTC TTCCGGCCCA ACTCTCCTTC CGCAGTGTAA TTTTGTATG	274
TGTGGATTAA GATGACTCTT GGTACTAACAA TACATTTCT GATTAAACCT ATCTGNACAT	334
GAGTTGTTT TATTTCTTAC CCTTTCCAG AGC GAT GAT TCT GAC ATT TGG GAT Ser Asp Asp Ser Asp Ile Trp Asp	387
30 35	
GAT ACA GCA CTG ATA AAA GCA TAT GAT AAA GCT GTG GCT TCA TTT AAG Asp Thr Ala Leu Ile Lys Ala Tyr Asp Lys Ala Val Ala Ser Phe Lys	435
40 45 50	
GTATGAAATG CTTGNTTAGT CGTTTCTTA TTTTCTCGTT ATTCAATTGG AAAGGAATTG	495
ATAACATACG ATAAAGTGTT AAAGGTGCTT TCTGAGGTGA CGGAGCCTTG AGACTAGCTT	555
ATAGTAGTAA CTGGGTTATG TCGTGACTTT TATTCTGTGC ACCACCTGT AACATGTACA	615
TTTTTATTCC TATTTTCGTA G CAT GCT CTA AAG AAT GGT GAC ATT TGT GAA His Ala Leu Lys Asn Gly Asp Ile Cys Glu	666
55 60	
ACT TCG GGT AAA CCA AAA ACC ACA CCT AAA AGA AAA CCT GCT AAG AAG Thr Ser Gly Pro Lys Thr Pro Lys Arg Lys Pro Ala Lys Lys	714
65 70 75	
AAT AAA AGC CAA AAG AAG AAT ACT GCA GCT TCC TTA CAA CAG Asn Lys Ser Gln Lys Asn Thr Ala Ala Ser Leu Gln Gln	756
80 85 90	
GTTATTTAA AATGTTGAGG ATTTAACTTC AAAGGATGTC TCATTAGTCC TTATTTAATA	816
GTGTAAAATG TCTTTAACTG CCTGCAGGTC GATCAAAACG AGATGATAGT TTGCCCTCTT	876
CAAAAGAAAT GTGTGCATGT ATATATCTTT GATTCTTT GTAG TGG AAA GTT GGG Trp Lys Val Gly	932
95	
GAC AAA TGT TCT GCC ATT TGG TCA GAA GAC GGT TGC ATT TAC CCA GCT Asp Lys Cys Ser Ala Ile Trp Ser Glu Asp Gly Cys Ile Tyr Pro Ala	980
100 105 110	
ACC ATT GCT TCA ATT GAT TTT AAG AGA GAA ACC TGT GTT GTG GTT TAC Thr Ile Ala Ser Ile Asp Phe Lys Arg Glu Thr Cys Val Val Val Tyr	1028
115. 120 125	

ACT GGA TAT GGA AAT AGA GAG GAG CAA AAT CTG TCC GAT CTA CTT TCC Thr Gly Tyr Gly Asn Arg Glu Glu Gln Asn Leu Ser Asp Leu Leu Ser 130 135 140	1076
CCA ATC TGT GAA GTA GCT AAT AAT ATA GAA CAG AAT GCT CAA GAG Pro Ile Cys Glu Val Ala Asn Asn Ile Glu Gln Asn Ala Gln Glu 145 150 155	1121
GTAAGGATAC AAAAAAAA AAATTCAATT TCTGGAAGCA GAGACTAGAT GAGAAACTGT	1181
TAAACAGTAT ACACCACCGA GGCATTAATT TTTCTTAAT CACACCTTA TAACAAAAAC	1241
CTGCATATTT TTTCTTTTA AAG AAT GAA AAT GAA AGC CAA GTT TCA ACA GAT Asn Glu Asn Glu Ser Gln Val Ser Thr Asp 160 165	1294
GAA AGT GAG AAC TCC AGG TCT CCT GGA AAT AAA TCA GAT AAC ATC AAG Glu Ser Glu Asn Ser Arg Ser Pro Gly Asn Lys Ser Asp Asn Ile Lys 170 175 180	1342
CCC AAA TCT GCT CCA TGG AAC TCT TTT CTC CCT CCA CCA CCC CCC ATG Pro Lys Ser Ala Pro Trp Asn Ser Phe Leu Pro Pro Pro Pro Pro Met 185 190 195 200	1390
CCA GGG CCA AGA CTG GGA CCA GGA AAG GTAAACCTTC TATGAAAGTT Pro Gly Pro Arg Leu Gly Pro Gly Lys 205	1437
TTCCAGAAAA TAGTTAATGT CGGGACATTT AACCTCTCTG TTAACTAATT TGTAGCTCTC	1497
CCACAAATAT TCTGGTAAT TATTTTATC CTTTGTTTG TGAGTCCTTT TTATTCCTAT	1557
CATATTGAAA TTGGTAAGTT AATTTCCCTT TGAAATATTC CTTATAG CCA GGT CTA Pro Gly Leu 210	1613
AAA TTC AAT GGC CCA CCA CCG CCA CCG CCA CCA CCA CCA CCC CAC TTA Lys Phe Asn Gly Pro Pro Pro Pro Pro Pro Pro Pro His Leu 215 220 225	1661
CTA TCA TGC TGG CTG CCT CCA TTT CCT TCT GGA CCA CCA GTAAGTAAAAA Leu Ser Cys Trp Leu Pro Pro Phe Pro Ser Gly Pro Pro 230 235 240	1710
AAGAGTATAG GTTAGATTTT GCTTCACAT ACAATTGAT AATTACCAGA CTTTACTTTT	1770
TGTTTACTGG ATATAAACAA TATCTTTTC TGTCTCCAG ATA ATT CCC CCA CCA Ile Ile Pro Pro Pro 245	1824
CCT CCC ATA TGT CCA GAT TCT CTT GAT GAT GCT GAT GCT TTG GGA AGT Pro Pro Ile Cys Pro Asp Ser Leu Asp Asp Ala Asp Ala Leu Gly Ser 250 255 260	1872
ATG TTA ATT TCA TGG TAC ATG AGT GGC TAT CAT ACT GGC TAT TAT ATG Met Leu Ile Ser Trp Tyr Met Ser Gly Tyr His Thr Gly Tyr Tyr Met 265 270 275	1920
GTAAGTAATC ACTCAGCATC TTTCTGAC AATTTTTTG TAGTTATGTG ACTTTGTTG	1980
GTAAATTAT AAAATACTAC TTGAAGTCA GCCTAATAAT TGTTTCTTT GGGATAACTT	2040

TTAAAGTACA TTAAAAGACT ATCAACTTAA TTTCTGATCA TATTTGTTG AATAAAATAA	2100
GTAAAATGTC TTGTGAAACA AAATGCTTT TAACATCCAT ATAAAGCTAT CTATATATAG	2160
CTATCTATGT CTATATAGCT ATTTTTTTA ACTTCCTTTT ATTTCCCTTA CAG GGT	2216
Gly	
TTC AGA CAA AAT CAA AAA GAA GGA AGG TGC TCA CAT TCC TTA AAT	2261
Phe Arg Gln Asn Gln Lys Glu Gly Arg Cys Ser His Ser Leu Asn	
280 285 290	
TAAGGAGTAA GTCTGCCAGC ATTATGAAAG TGAATCTTAC TTTTGTAAAA CTTTATGGTT	2321
TGTGGAAAAC AAATGTTTT GAACAGTTAA AAAGTTCAGA TGTTAAAAAG TTGAAAGGTT	2381
AATGTAAAAC AATCAATATT AAAGAATTTT GATGCCAAAA CTATTAGATA AAAGGTTAAT	2441
CTACATCCCT ACTAGAATTC TCATACTTAA CTGGTTGGTT ATGTGGAAGA AACATACTT	2501
CACAATAAAG AGCTTTAGGA TATGATGCCA TTTTATATCA CTAGTAGGCA GACCAGCAGA	2561
CTTTTTTTA TTGTGATATG GGATAACCTA GGCATACTGC ACTGTACACT CTGACATATG	2621
AAGTGCTCTA GTCAAGTTA ACTGGTGTCC ACAGAGGACA TGGTTTAAC GGAATTCGTC	2681
AAGCCTCTGG TTCTAATTTC TCATTCAG GAAATGCTGG CATAGAGCAG CACTAAATGA	2741
CACCACTAAA GAAACGATCA GACAGATCTG GAATGTGAAG CGTTATAGAA GATAACTGGC	2801
CTCATTCTT CAAAATATCA AGTGTGGGA AAGAAAAAAG GAAGTGAAT GGGTAACTCT	2861
TCTTGATTAA AAGTTATGTA ATAACCAAAT GCAATGTGAA ATATTTACT GGACTCTTT	2921
GAAAACCAT CTAGTAAAAG ACTGGGTGG GGGTGGGAGG CCAGCACGGT GGTGAGGCAG	2981
TTGAGAAAAT TTGAATGTGG ATTAGATTAA GAATGATATT GGATAATTAT TGGTAATTT	3041
ATGGCCTGTG AGAAGGGTGT TGTAGTTAT AAAAGACTGT CTTAATTGC ATACTTAAGC	3101
ATTTAGGAAT GAAGTGTAG AGTGTCTTAA AATGTTCAA ATGGTTAAC AAAATGTATG	3161
TGAGGCGTAT GTGGCAAAAT GTTACAGAAT CTAACTGGTG GACATGGCTG TTCATTGTAC	3221
TGTTTTTTTC TATCTTCTAT ATGTTAAAAA GTATATAATA AAAATATTTA	3271

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 637 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATCTGCCTT CCTTCCTGCC CCCATGTTG TCTTCCTTG TTTGTCTTA TATAGATCAA	60
GCAGGTTTA AATTCTAGT AGGAGCTTAC ATTACTTT CCAAGGGGA GGGGAATAA	120
ATATCTACAC ACACACACAC ACACACACCA CACTGGAGTT CGAGACGAGG CCTAAGCAAC	180
ATGCCGAAAC CCCGCTCTA CTAAATACAA AAAATAGCTG AGCTTGGTGG CGCACGCCTA	240
TAGTCCTAGC TACTGGGAG GCTGAGGTGG GAGGATCGCT TGAGCCAAG AAGTCGAGGC	300
TGCAGTGAGC CGAGATCGCG CCGCTGCACT CCAGCCTGAG CGACAGGGCG AGGCTCTGTC	360
TCAAAACAAA CAAACAAAAA AAAAAAGGAA AGGAAATATA ACACAGTGAA ATGAAAGGAT	420
TGAGAGAAAT GAAAAATATA CACGCCACAA ATGTGGGAGG GCGATAACCA CTCGTAGAAA	480
CGGTGAGAAG TTACTACAAG CGGTCTCCC GGGCACCGTA CTGTTCCGCT CCCAGAACCC	540
CCGGGCGCCG GAAGTCGTCA CTCTTAAGAA GGGACGGGGC CCCACGCTGC GCACCCGCGG	600
GTTCGCTATG GCGATGAGCA GCGCGGGCAG TGGTGGC	637

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AGGGCGAGGC TCTGTCTCA

19

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGGGAGGACC GCTTGTAGT

19

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCCGGAAGTC GTCACTCTT

19

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGGTGCTGAG AGCGCTAATA

20

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TGTGTGGATT AAGATGACTC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CACTTTATCG TATGTTATC

19

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTGTGCACCA CCCTGTAAACA TG

22

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAGGACTAAT GAGACATCC

19

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGAGATGATA GTTGCCCTC

20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGCTACTTCA CAGATTGGGG AAAG

24

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCATCTAGT CTCTGCTTCC

20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGGATATGGA AATAGAGAGG GAGC

24

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CACCCTTATA ACAAAAACCT GC

22

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAGAAAGGAG TTCCATGGAG CAG

23

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAGAGGTTAA ATGTCCCGAC 20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTGAGAACTC CAGGTCTCCT GG 22

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TGAGTCTGTT TGACTTCAGG 20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAAGGAAATG GAGGCAGCCA GC

22

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TTTCTACCCA TTAGAACATCTG G

21

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCCACTTAC TATCATGCTG GCTG

24

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCAGACTTTA CTTTTGTTT ACTG

24

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATAGCCACTC ATGTACCATG A

21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAGAGTAATT TAAGCCTCAG ACAG

24

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTCCCATATG TCCAGATTCT CTTG

24

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AGACTATCAA CTTAATTCT GATCA

25

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TAAGGAATGT GAGCACCTTC CTTC

24

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGACTATCAA CTTAATTCT GATCA

25

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTAAGATTCA CTTTCATAAT GCTG

24

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTTTATGGTT TGTGGAAAAC A

21

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCATCATAT CCTAAAGCTC

20

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTAATAACCA AATGCAATGT GAA

23

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTACAAACACC CTTCTCACAG

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGTGTCCACA GAGGACATGG

20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AAGAGTTAAC CCATTCCAGC TTCC

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ser Asp Asp Ser Asp Ile Trp Asp Asp Thr Ala Leu Ile Lys Ala Tyr
 1 5 10 15
 Asp Lys Ala Val Ala Ser Phe Lys
 - 20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

His	Ala	Leu	Lys	Asn	Gly	Asp	Ile	Cys	Glu	Thr	Ser	Gly	Lys	Pro	Lys
1									10					15	
Thr	Thr	Pro	Lys	Arg	Lys	Pro	Ala	Lys	Lys	Asn	Lys	Ser	Gln	Lys	Lys
														30	
Asn	Thr	Ala	Ala	Ser	Leu	Gln	Gln								
								35	40						

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Trp	Lys	Val	Gly	Asp	Lys	Cys	Ser	Ala	Ile	Trp	Ser	Glu	Asp	Gly	Cys
1					5					10					15
Ile	Tyr	Pro	Ala	Thr	Ile	Ala	Ser	Ile	Asp	Phe	Lys	Arg	Glu	Thr	Cys
					20				25					30	
Val	Val	Val	Tyr	Thr	Gly	Tyr	Gly	Asn	Arg	Glu	Glu	Gln	Asn	Leu	Ser
						35		40				45			
Asp	Leu	Leu	Ser	Pro	Ile	Cys	Glu	Val	Ala	Asn	Asn	Ile	Glu	Gln	Asn
						50		55				60			
Ala	Gln	Glu													
	65														

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asn	Glu	Asn	Glu	Ser	Gln	Val	Ser	Thr	Asp	Glu	Ser	Glu	Asn	Ser	Arg
1					5				10					15	
Ser	Pro	Gly	Asn	Lys	Ser	Asp	Asn	Ile	Lys	Pro	Lys	Ser	Ala	Pro	Trp
						20			25					30	
Asn	Ser	Phe	Leu	Pro	Pro	Pro	Pro	Pro	Met	Pro	Gly	Pro	Arg	Leu	Gly
						35			40			45			
Pro	Gly	Lys													
	50														

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Pro Gly Leu Lys Phe Asn Gly Pro Pro Pro Pro Pro Pro Pro Pro
 1 5 10 15

Pro His Leu Leu Ser Cys Trp Leu Pro Pro Phe Pro Ser Gly Pro Pro
 20 25 30

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ile Ile Pro Pro Pro Pro Ile Cys Pro Asp Ser Leu Asp Asp Ala
 1 5 10 15

Asp Ala Leu Gly Ser Met Leu Ile Ser Trp Tyr Met Ser Gly Tyr His
 20 25 30

Thr Gly Tyr Tyr Met
 35

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gly Phe Arg Gln Asn Gln Lys Glu Gly Arg Cys Ser His Ser Leu Asn
 1 5 10 15

50

85